

Resource Summary Report

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Chinese Glioma Genome Atlas

RRID:SCR_018802

Type: Tool

Proper Citation

Chinese Glioma Genome Atlas (RRID:SCR_018802)

Resource Information

URL: <http://www.cgga.org.cn/>

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Description: Web application for data storage and analysis to explore brain tumors datasets from Chinese cohorts. Data portal for storage and interactive exploration of multi-dimensional functional genomic data that includes primary and recurrent glioma samples from Chinese cohorts. Allows users to browse DNA mutation profile, mRNA/microRNA expression profile and methylation profile, and to do correlation and survival analysis in specific glioma subtype.

Abbreviations: CGGA

Resource Type: data or information resource, data set, database, disease-related portal, portal, topical portal

Defining Citation: [DOI:10.1101/2020.01.20.911982](https://doi.org/10.1101/2020.01.20.911982)

Keywords: Functional genomic data, glioma samples, brain tumor datasets, Chinese cohort, whole exome sequencing data, DNA methylation data, mRNA sequencing data, microRNA microarray data, clinical data, DNA mutation profile analysis, expression profile, methylation profile, survival analysis, glioma subtype, FASEB list

Related Condition: Glioma

Availability: Free, Freely available

Resource Name: Chinese Glioma Genome Atlas

Resource ID: SCR_018802

Record Creation Time: 20220129T080342+0000

Record Last Update: 20260912T195906+0000

Ratings and Alerts

No rating or validation information has been found for Chinese Glioma Genome Atlas.

No alerts have been found for Chinese Glioma Genome Atlas.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1344 mentions in open access literature.

Listed below are recent publications. The full list is available at [Kravitz](#) .

Wu N, et al. (2026) Arginine deprivation enhances ASS1-negative glioblastoma radiosensitivity via epigenetic silencing of DNA repair genes. *Cell death & disease*.

Ding C, et al. (2026) Glioblastoma-Secreted C1QL1 Orchestrates Tumor Microtube Expansion and Neural Synaptic Pruning to Drive Malignant Synapse Formation and Recurrence. *Cancer discovery*, 16(6), 1176.

Xiong K, et al. (2026) Multimodal-based analysis of single-cell ATAC-seq data enables highly accurate delineation of clinically relevant tumor cell subpopulations. *Genome medicine*, 18(1), 19.

Hou Z, et al. (2026) Impact of extent of surgical resection on survival in World Health Organization grade 4 gliomas: A molecular subtype-based analysis. *Neuro-oncology advances*, 8(1), vdaf204.

Jia Z, et al. (2026) Engrailed 1 promotes immune evasion and chemoresistance in glioma through single cell and CeRNA network analyses. *Scientific reports*, 16(1), 4913.

Zhang Z, et al. (2026) Machine learning model on multi-omics data enables risk stratification and identifies molecular heterogeneity and therapeutic targets in glioblastoma. *Molecular cancer*, 25(1).

Lin S, et al. (2026) Clinical significance and oncogenic role of ECHDC2 in glioblastoma: a comprehensive analysis based on bioinformatics and in vitro experiments. *Frontiers in genetics*, 17, 1759463.

Wu H, et al. (2026) Harnessing ?? T cells for B7-H3-targeting CAR therapy to enhance anti-tumor therapy in glioblastoma. *Journal of translational medicine*, 24(1).

Bao Z, et al. (2026) Vebreltinib for Previously Treated Astrocytoma, IDH-Mutant, Grade 4, and Glioblastoma, IDH Wild-Type with PTPRZ1-MET Fusion Gene: A Multicenter, Phase III Randomized, Open-Label Trial. *Cancer communications (London, England)*, 46, 0019.

- Ming W, et al. (2026) PSMC4 promotes low-grade glioma progression and predicts poor prognosis. *European journal of medical research*, 31(1).
- Sonpatki P, et al. (2026) A spatially resolved human glioblastoma atlas reveals distinct cellular and molecular patterns of anatomical niches. *Nature communications*, 17(1).
- Xu Z, et al. (2026) Hypoxia-induced BTN3A2 promotes glioma progression and chemoresistance via AKT/SP1/RAD51-mediated DNA damage. *Cell death & disease*, 17(1).
- Wang K, et al. (2026) Integrating multiomics to elucidate the role of chromatin remodeling in glioma and the antitumor mechanisms and therapeutic potential of targeting LMNA. *Frontiers in immunology*, 17, 1759811.
- Li J, et al. (2026) Multi-Omic Analysis of Glioma Identifies RRM2 as a Prognostic Biomarker Associated With Tumor Stemness and Cell Cycle-Related Pathways. *Technology in cancer research & treatment*, 25, 15330338261453490.
- Zhang J, et al. (2026) PDIA3 Inhibition Facilitates Sensitivity of IKE-Induced Ferroptosis via STAT3/LCN2 Axis to Improve Glioblastoma Therapy. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 13(12), e14191.
- Li Z, et al. (2026) A prognostic gene signature derived from aging-related genes predicts survival, immune landscape and therapy response in glioma. *Molecular and clinical oncology*, 24(1), 9.
- Le Joncour V, et al. (2026) Therapeutic Reprogramming of Glioblastoma Phenotypic States Using Multifunctional Heparin Nanoparticles. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 13(3), e09590.
- Cao Y, et al. (2026) CTSZ-dependent anoikis resistance enhances malignant characters of glioblastoma via NF- κ B signaling. *iScience*, 29(6), 115992.
- Liu X, et al. (2026) Structural dynamics of microtubules in glioma: impact on macrophage M2 polarization and tumor cell heterogeneity. *Journal of translational medicine*, 24(1).
- Zou X, et al. (2026) Down-regulation of circ0001361 induces apoptosis and suppresses the progression of glioma. *PloS one*, 21(4), e0343681.